



SEQUENCE LISTING

<110> Hresko, Michelle Coutu
McLaird, Merry B.
Williams, Deryck J.
Frevert, Anita M.
Chiapelli, Brandi
Baublite, Catherine
Kloek, Andrew P.
Davila-Aponte, Jennifer A.
Bradley, John D.
Xu, Siquan

<120> NEMATODE PAN AND ZP RECEPTOR-LIKE
SEQUENCES

<130> 12557-015001

<140> US 10/771,708

<141> 2004-02-04

<150> US 60/444,771

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Ile Phe Leu Ile Ser Thr Asn Ile Ala Ser Lys Ile Ser Gly Val Pro

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Leu Cys Asn Lys Asp Thr Ser Pro Val Phe Thr Leu Gln His Asn Ser

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Thr Pro Thr Asp Glu Thr Ser Ile Leu Leu Thr Lys Ser Cys Val Lys			
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Tyr Ala Pro Tyr Ile Thr Gln Tyr Ile Ala Val Glu Asn Lys Gln Ile			
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Cys Lys Ser Phe Met Tyr Asn Pro Glu Thr Lys Val Cys Tyr Leu Ser			
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gat gaa cgt tca aag cct ctt gga cgg gct aaa tta agt gat gct aat		926	
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275	280	285	
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Asp Ile Leu Glu Leu Arg Trp Glu Ile Met Ala Met Asp Glu Glu Leu	
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Gly Asp Glu Lys Leu Gln Leu Ile Glu Gly Gly Cys Pro Thr Pro Ala	
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Val Ala Gln Lys Leu Ile Pro Gln Pro Ile Lys Leu Gln Ser Ser Ala	
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Val Lys Ile Ala His Leu Gln Ala Phe Arg Phe Asp Ser Ser Ser Ser	
960 965 970	
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Tyr Lys Val Pro Arg Phe Ser Gln Ala Thr Thr Ser Leu Leu Ile Leu				
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Lys Ile Thr Asn				
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		125	
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495 500 505	
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510 515 520 525	
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Gly Ile Val Ser Met Ala Met Ile Cys Leu Leu Leu Ser Val Leu Ile	
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Val Met Trp Gly Cys His Ser Leu Asn Gln Ser Ser Lys Leu Pro Met	
545 550 555	

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Arg Ile Cys Ser Ser Pro Phe His Phe Asp Val Tyr Glu Gln Lys Ile	
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Val Val Tyr Tyr Leu Asp Ser Asn	Cys	Ala	Gly	Ser	Gln
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Pro Tyr Ile Thr Gln Tyr Ile	Ala	Val	Glu	Asn	Lys
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Leu Cys Thr Gly Arg Ile Thr Val	Thr	Gln	Asn	Asp	Phe
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Ser Phe Met Tyr Asn Pro Glu Thr	Lys	Val	Cys	Tyr	Leu
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Thr Pro Ser Phe Asn Arg Val Pro	Gln	Met	Ile	Leu	Val
305	310				Gly
Ala Phe Val Met Glu Asn Val Pro	Ser	Val	Thr	Met	Cys
325	330				Leu
Cys Thr Asn Pro Pro Pro Glu Thr	Gly	Gl	Lys	Phe	Val
340	345				Cys
Val Met Tyr Tyr Tyr Asn Glu Gln	Glu	Cys	Ile	Leu	Asn
355	360				Ala
Arg His Thr Lys Pro Asp Leu Phe	Ile	Thr	Glu	Gly	Asp
370	375				Glu
Val Asp Tyr Phe Asp Ile Ser Cys	His	Leu	Glu	Pro	Glu
385	390				Thr
Lys Gly Thr Tyr Leu Lys Gly Ile	Lys	Ser	Ile	Asn	Ser
405	410				Ala
Glu Gly Glu Gly Ser Leu His Val	Ile	Glu	Ser	Ala	Gly
420	425				Lys
Glu Glu Cys Met Glu Lys Cys Asn	Gln	Leu	His	Pro	Ser
435	440				Leu
Ser Phe Asn Phe Glu Lys Ser Ser	Gly	Leu	Cys	Asn	Cys
450	455				Arg
Asp Gly Lys Asn Thr Leu Lys Pro	Phe	Ile	Lys	Asn	Gly
465	470				Phe
Val Asp Leu Gln Cys Leu Ser Thr	Lys	Lys	Asp	Cys	Asp
485	490				Leu
Asn Asp Ile Asn Phe Val Lys Tyr	Leu	Tyr	Ser	His	Val
500	505				Lys
Leu Tyr Ser Gln Gln Pro Gly Ile	Pro	Thr	Lys	Thr	Tyr
515	520				Ile
Gly Ile Ser Lys Cys Leu Asp Leu	Cys	Thr	Asp	Ser	Glu
530	535				Arg
Gly Leu Asn Tyr Asn Arg Arg Thr	Gly	Glu	Cys	Glu	Cys
545	550				Glu
Ile Asp Gly Pro Ser Asn Leu Lys	Ser	Glu	His	Ile	Phe
565	570				Tyr
Gln Asn Leu Cys Ser Thr Lys Glu	Asn	Glu	Ala	Gly	Val
580	585				Ser
Leu Asn Val Pro Gln Ser Ser Val	Ile	Pro	Ile	Ser	Ser
595	600				Gln
Ile Ser Lys Ser Asp Val Phe Ala	Lys	Lys	Asn	Leu	Asn
610	615				Gly
					620

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 Gly Ser Lys Asn Glu Thr Ser Tyr Glu Thr Gly Thr Val Asn Lys Ser
 645 650 655
 Asn Val Glu Glu Val Ser Glu Thr Leu Thr Asn Ser Gly Val Glu Ser
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 675 680 685
 Ile Pro Glu Gly Pro Leu Pro Val Pro Ile Leu Ile Pro Ala Asp Gln
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 Pro Gln Ser Phe Thr Gly Val Ile Phe Val Lys Asn His Tyr Glu Thr
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 Cys Arg Val Glu Val Ser Asn Ser Asp Ala Ala Thr Leu Glu Leu Gly
 740 745 750
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 755 760 765
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 770 775 780
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 835 840 845
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 Phe Val Lys Asp Cys His Ala Glu Pro Gly Thr Gly Ala Gly Gly Asp
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 945 950 955 960
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 965 970 975
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 Cys Asp Met His Gly Glu Ser Lys Gln Ser Trp Gly Arg Lys Lys Arg
 995 1000 1005
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 1060 1065 1070
 Glu Thr Ala His Leu Asn Gly Asn Leu Cys Met Gly Lys Ile Thr Leu

1075	1080	1085
Phe Ser Val Phe Gly Val	Leu Leu Ser Leu Ile Val Val Gln Ala Ile	
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Val Val Thr Asn Tyr Ile	Phe Lys Arg Val Met Ser Ser Arg Lys Ile	
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Thr Asn		1120

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Arg Ile Ser Arg Ala Arg Leu Asp Gly Thr Pro Val Val Ile Ser Thr			
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Ala Gly His Asp Leu Thr Cys Ala Gln Tyr Cys Arg Asn Asn Ile Glu			
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Pro Thr Thr Gly Ala Gln Arg Val Cys Ala Ser Phe Asn Phe Asp Gly			
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Arg Glu Thr Cys Tyr Phe Phe Asp Asp Ala Ala Ser Pro Ala Gly Thr			
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Gly Glu Leu Asn Glu Ala Pro Ser Ala Asn Asn Phe Tyr Tyr Glu Lys			
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Val Cys Leu Pro Ala Ile Ser Ala His Glu Ala Cys Thr Tyr Arg Ser			
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Phe Ser Phe Glu Arg Thr Arg Asn Thr Gln Leu Glu Gly Phe Val Lys			
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145	150	155	160
Lys Glu Ser Glu Phe Val Cys Arg Ser Val Asn Tyr Asn Tyr Glu Asn			
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Phe Met Cys Glu Leu Ser Thr Glu Arg Ser Arg Ser Lys Pro Gln Asn			
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Met Arg Met Ser Ala Ala Pro Val Asp Tyr Tyr Asp Asn Asn Cys Leu			
195	200	205	
Asn Arg Gln Asn Arg Cys Gly Glu Ser Gly Gly Asn Leu Ile Phe Ile			
210	215	220	
Lys Thr Thr Gln Phe Glu Ile His Tyr Tyr Asp His Thr Gln Ser Met			
225	230	235	240
Glu Ala Gln Glu Ser Phe Cys Leu Gln Lys Cys Leu Asp Ser Leu Asn			
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Thr Phe Cys Arg Ser Val Glu Tyr Ser Pro Ser Glu Lys Asn Cys Ile			
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Val Ser Asp Glu Asp Thr Tyr Ser Arg Ala Asp Gln Gln Gly Glu Val			
275	280	285	
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Ser Ser Thr Cys Arg Gln Gln Ala Ala Phe Glu Arg Phe Ile Gly Ser			
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370						375				380					
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Leu	Gln	Asp	Phe	Asp	Lys	Asn	Arg	Leu	Lys	Ser	Glu	Met	Lys	Ala	Phe
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Cys	Ala	Gly	Pro	Met	Gly	Cys	Pro	Pro	Ser	Asn	Cys	Leu	Asp	Ser	Gly
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Thr	Asn	Glu	Leu	Phe	Ala	Ser	His	Gly	Arg	Lys	Lys	Arg	Ser	Ile	Val
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Asp	Phe	Lys	Asn	Thr	Thr	Ser	Ala	Glu	Thr	Leu	Ser	Ala	Ile	Ile	
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Arg	Val	Leu	Ala	Ala	Gly	Glu	Glu	Glu	Leu	Glu	Val	Glu	Glu	Phe	Tyr
						485		490						495	
Arg	Asn	Asp	Thr	Asn	Phe	Lys	Tyr	Asp	Ser	Glu	Glu	Asn	Ile	Ser	Ala
						500			505				510		
His	Asn	Leu	Tyr	Cys	Met	Ser	Glu	Met	Trp	Phe	Val	Ser	Gly	Ile	Val
						515		520				525			
Ser	Met	Ala	Met	Ile	Cys	Leu	Leu	Leu	Ser	Val	Leu	Ile	Val	Met	Trp
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attgattgtt cagaacattt ttcctttcg ttagattgtt ttggcggttga atattggcagg 240
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Leu Phe Thr Phe Leu Thr Thr Lys Cys Gln Ala Tyr Ser Ile Pro Leu	
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Ile Ser Glu Cys Asn Ser Glu Glu Ala Pro Val Phe Leu Leu Gln Arg	
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85 90 95	
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Lys Thr Thr Met Thr Ala Thr Leu Ser Leu Gln Asp Ile Asn Leu	
100 105 110	
aca cta gct aga tta gct act aaa agt tgt gtt aag agc aaa aca atc	564
Thr Leu Ala Arg Leu Ala Thr Lys Ser Cys Val Lys Ser Lys Lys Ile	
115 120 125	

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Gly Phe Ala Arg Glu Val Val Ser Ala Glu Ser Ile His Gln Cys Leu	
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Arg Leu Asp Arg Pro Asp Leu Phe Val Asp Glu Lys Glu Asp Thr Val	
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Val Tyr Leu Asp Asn Asn Cys Ala Gly Ser Gln Cys His Ala Pro Tyr	
210 215 220	
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Val Thr Gln Tyr Val Ala Val Glu Gly Lys Gln Leu Ala Glu Glu Leu	
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325 330 335	
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340 345 350	

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gtt cat tgt ttg agt gga aca tct caa ctt tta gga gaa aat tct aaa Val His Cys Leu Ser Gly Thr Ser Gln Leu Leu Gly Glu Asn Ser Lys 500 505 510	1716
cat tct ccc tct gct tgt gtt gac cca gaa ggg gct att ttt agt cgt His Ser Pro Ser Ala Cys Val Asp Pro Glu Gly Ala Ile Phe Ser Arg 515 520 525	1764
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Phe Thr Ser Leu Leu Leu Asn Ser Ser Pro Asn Ser Gln Gln Asp Lys			
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Asp Glu His Val Asp Phe Tyr Arg Asn Ile Cys Arg Val Lys Glu Ser			
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Asp Asp Gly Glu Asn Ser Ile Thr Gly Thr Ala Pro Pro Pro Val Asp			
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Gly Lys Leu Ile Ile Lys Pro Ser Pro Gln Val Ser Ile Pro Ser Pro			
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755	760	765	
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Ala Leu Phe Trp Phe Trp Gly Phe Gln Gln Ile Leu Glu Met Lys Pro			
770	775	780	
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Ile Ala Leu Ile Asn Ser Gln Lys His Gly Lys Gly Asn Lys Thr His			
785	790	795	800
gga gat act tta ctt tct att gaa ggt tcc aaa aaa caa att gaa ggg		2628	
Gly Asp Thr Leu Leu Ser Ile Glu Gly Ser Lys Lys Gln Ile Glu Gly			

805	810	815	
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aaa cgt tca aga aga caa tta caa aga gat tgt gga tta caa gat atg Lys Arg Ser Arg Arg Gln Leu Gln Arg Asp Cys Gly Leu Gln Asp Met 835	840	845	2724
gac aat gga act tac aaa act gtt att gtt gtc caa aca aat aat ttg Asp Asn Gly Thr Tyr Lys Thr Val Ile Val Val Gln Thr Asn Asn Leu 850	855	860	2772
gga att ccg gga ctt gtt act tct atg gac caa ctt tat gag att tcc Gly Ile Pro Gly Leu Val Thr Ser Met Asp Gln Leu Tyr Glu Ile Ser 865	870	875	2820
tgt aac tat tca agt atg ttg gga ggc aaa gtc caa aca gca gct gca Cys Asn Tyr Ser Ser Met Leu Gly Gly Lys Val Gln Thr Ala Ala Ala 885	890	895	2868
tta cgt gtt cac ggt ccc caa cct tca cta atc cag cct cgc ggc aaa Leu Arg Val His Gly Pro Gln Pro Ser Leu Ile Gln Pro Arg Gly Lys 900	905	910	2916
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gaa agg caa agt ggg gaa ggg cct tta att caa gct aaa ttg ggg gat Glu Arg Gln Ser Gly Glu Gly Pro Leu Ile Gln Ala Lys Leu Gly Asp 930	935	940	3012
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Asn Cys Lys Phe Asn Asp Gly Ile Lys Glu Ser Trp Gly Arg Lys Arg	
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Arg Phe Ala Ile Asp Asn Asn Ile Asn Arg Lys Asn Glu Val Lys Glu	
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Phe Glu Thr Arg Arg Phe Val Val Pro Arg Phe Ala Gln Ala Thr Thr	
1075 1080 1085	
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Ser Leu Val Ile Val Asp Pro Leu Gln Gln Asn Ser Val Ile Lys	
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Thr Glu Gln Gln Gln Pro Phe Ile Ser His Ser Ser Ile Ser Lys	
1105 1110 1115 1120	
caa ata ttt gaa aat aat aaa aaa gaa aat aat aaa aat ata aca aaa	3588
Gln Ile Phe Glu Asn Asn Lys Lys Glu Asn Asn Lys Asn Ile Thr Lys	
1125 1130 1135	
aca gct aaa aaa tcc tct tct ctt ttt gaa gct ttt act gag gct gct	3636
Thr Ala Lys Lys Ser Ser Leu Phe Glu Ala Phe Thr Glu Ala Ala	
1140 1145 1150	
ggt gga agg aaa att aat tta gaa tta aca aca aca aat tca gaa caa	3684
Gly Gly Arg Lys Ile Asn Leu Glu Leu Thr Thr Asn Ser Glu Gln	
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Gln Gln Leu Cys Leu His Lys Trp Thr Leu Gly Gly Val Phe Gly Thr	
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Leu Leu Thr Leu Ile Val Val Gln Ser Gly Val Ala Ala Lys His Leu	
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att ttg aac acg gag gac cga ttg gat cgg cct gac ctt ttc gtg gac Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe Val Asp 50 55 60	192
gag cac gag gac acg gtc atc tac ttg gac aac aat tgc gcc gga tgt Glu His Glu Asp Thr Val Ile Tyr Leu Asp Asn Asn Cys Ala Gly Cys 65 70 75 80	240
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gac caa caa ttc gca att gca gca caa tgt tac gca ccg tac gta acg Asp Gln Gln Phe Ala Ile Ala Ala Gln Cys Tyr Ala Pro Tyr Val Thr 100 105 110	336
caa tac gtg gcg gtg gaa gga cgc caa ttg tcg gac gaa ttg gac cac Gln Tyr Val Ala Val Glu Gly Arg Gln Leu Ser Asp Glu Leu Asp His 115 120 125	384
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Met His Leu Ser				
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Asn His Ala Ser Ser Leu Leu His Tyr Tyr Ser His Leu Ile Ile Ile				
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Ala Tyr Phe Ser Val Phe Ala Ser Ile Glu Ile Gln Glu Ile Pro Ser				
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Tyr Pro Ala Cys Ser Asn Gly Glu Ser Pro Val Phe Leu Leu Gln His				
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Thr Gly His Leu Asn Asp Tyr Val Leu Leu Ser Lys Asn Cys Ala Lys				
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Ser Ala Arg Ile Cys Ser Ser Pro Phe Gln Phe Asp Val His Arg Gln				
120 125 130				
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Lys Ile Leu Val Gly Phe Ala Arg Glu Val Val Ser Ala Asp Ser Leu			
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Ser Leu Cys Leu Ser Ala Cys Leu Asn Ala Phe Asp Ser Phe Gly Phe			
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Glu Cys Glu Ser Val Met Tyr Tyr Pro Val Asp Ser Glu Cys Ile Leu			
165	170	175	180
aac acc gaa gat cgt ctg gat cga cct gac ttg ttt ggg gat gaa tta			753
Asn Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe Gly Asp Glu Leu			
185	190	195	
gat gat aac gtc att tat ttg gat aac aac tgt gct gga tca cag tgt			801
Asp Asp Asn Val Ile Tyr Leu Asp Asn Asn Cys Ala Gly Ser Gln Cys			
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tat gct cca tac ata aca caa tac att gcc gtc gca aat cgt cag cta			849
Tyr Ala Pro Tyr Ile Thr Gln Tyr Ile Ala Val Ala Asn Arg Gln Leu			
215	220	225	
gct aac gag ttg gac aga caa ctg atc gct gat cgt gaa tca tgc gag			897
Ala Asn Glu Leu Asp Arg Gln Leu Ile Ala Asp Arg Glu Ser Cys Glu			
230	235	240	
tcg tta tgt act cag cga ctg tct aca acg aca aac gat ttc aac tgt			945
Ser Leu Cys Thr Gln Arg Leu Ser Thr Thr Asn Asp Phe Asn Cys			
245	250	255	260
aaa tca ttt atg cat aat ccg gaa act aac gtt tgc ata ctt tct gat			993
Lys Ser Phe Met His Asn Pro Glu Thr Asn Val Cys Ile Leu Ser Asp			
265	270	275	
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Glu Arg Ser Lys Pro Leu Gly Arg Gly Asn Leu Val Lys Ala Asp Gly			
280	285	290	
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Ala Ala Phe Val Met Glu Asn Val Pro Ser Val Thr Met Cys Leu Asp			
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cag tgc aca aat cct cca ccg gaa act gga gaa aat ttc gaa tgc aaa			1233
Gln Cys Thr Asn Pro Pro Glu Thr Gly Glu Asn Phe Glu Cys Lys			
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Ser Val Met Tyr Tyr Asn Glu Gln Glu Cys Ile Leu Asn Ala Glu			

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Cys Ser Ser Pro Phe His Phe Asp Val His Glu Gln Lys Ile Leu Val	
130 135 140	
Gly Phe Ala Arg Glu Val Val Ser Ala Glu Ser Ile His Gln Cys Leu	
145 150 155 160	
Thr Ala Cys Leu Asp Ala Val Asp Thr Phe Gly Phe Glu Cys Glu Ser	
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Val Met Tyr Tyr Pro Leu Asp Ala Glu Cys Ile Leu Asn Thr Glu Asp	
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Arg Leu Asp Arg Pro Asp Leu Phe Val Asp Glu Lys Glu Asp Thr Val	
195 200 205	
Val Tyr Leu Asp Asn Asn Cys Ala Gly Ser Gln Cys His Ala Pro Tyr	
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Val Thr Gln Tyr Val Ala Val Glu Gly Lys Gln Leu Ala Glu Glu Leu	
225 230 235 240	
Asp His Asn Phe Glu Gly Met Glu Leu Thr Glu Cys Glu Gln Leu Cys	
245 250 255	
Asn Gln Arg Leu Ser Val Ser Ala Asn Asp Phe Asn Cys Lys Ala Phe	
260 265 270	

Met Tyr Asn Asn Gln Thr Arg Ser Cys Ile Leu Ser Asp Glu Arg Ser
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 Arg Pro Leu Gly Arg Ala Asn Leu Thr Asp Ala Lys Gly Trp Thr Tyr
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 His Glu Lys Lys Cys Phe Ala Ser Pro Arg Thr Cys Arg Asn Val Pro
 305 310 315 320
 Ser Phe Thr Arg Val Pro Gln Met Leu Leu Val Gly Phe Ala Ser Phe
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 Val Met Glu Asn Val Pro Ser Val Thr Met Cys Leu Asp Gln Cys Thr
 340 345 350
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 Tyr Tyr Asn Glu Gln Glu Cys Ile Leu Asn Ala Glu Ser Arg His
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 Ser Lys Pro Asp Leu Phe Ile Pro Glu Glu Asp Asp Phe Val Val Asp
 385 390 395 400
 Tyr Phe Asp Ile Asn Cys Arg Leu Glu Gln Glu Gln Cys Ile Asp Gly
 405 410 415
 Arg Thr Pro Gln Leu Val Arg Thr Ile Asn Ser Ala Leu Pro Glu Gly
 420 425 430
 Glu Gly Ser Ile His Val Leu Glu Thr Ile Lys Gly Gly Val Gln Gln
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 Cys Ala Lys Lys Cys Ser Glu Arg Ala Pro Asp Lys Cys Arg Ser Phe
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 Asn Phe Asp Lys Gln Ala Gly Asn Cys Asn Leu Leu Tyr Leu Asp Gly
 465 470 475 480
 Gln Gly Ser Leu Arg Pro Glu Gln Lys Thr Gln Phe Asp Leu Tyr Asp
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 Val His Cys Leu Ser Gly Thr Ser Gln Leu Leu Gly Glu Asn Ser Lys
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 His Ser Pro Ser Ala Cys Val Asp Pro Glu Gly Ala Ile Phe Ser Arg
 515 520 525
 Phe Leu Tyr Thr Arg Trp Val Ala Asn Ser Pro Asn Arg Glu Ile Ser
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 Ser Leu Pro Leu Ser Lys Cys Leu Asn Leu Cys Ser Val Gly Gly Glu
 545 550 555 560
 Gln Cys Glu Gly Val Asn Tyr Asn Arg Arg Asn Gly Ser Cys Gln Leu
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 Phe Thr Ser Leu Leu Asn Ser Ser Pro Asn Ser Gln Gln Asp Lys
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 Asp Glu His Val Asp Phe Tyr Arg Asn Ile Cys Arg Val Lys Glu Ser
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 Lys Ser Asp Ser Gly Ala Ala Asn Val Pro Lys Thr Gln Gln Ala Thr
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 Ala Ala Pro Pro Pro Ser Val Gln Leu Thr Thr Lys Pro Pro Gln Ile
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 Arg Asp Leu Asn Asn Asn Asn Lys Thr Thr His Lys Glu Pro Asn Ile
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 Lys Leu Pro Pro Gln Ser Ala Lys Pro Ile Asn Gly Lys Thr Gly Lys
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 Glu Gln Leu Pro Val Gly Ser Lys Ser Phe Gly Val Thr Asn Thr Arg
 675 680 685
 Asp Asp Gly Glu Asn Ser Ile Thr Gly Thr Ala Pro Pro Pro Val Asp
 690 695 700
 Gly Lys Leu Ile Ile Lys Pro Ser Pro Gln Val Ser Ile Pro Ser Pro
 705 710 715 720
 Val Leu Ile Pro Ala Gln Glu Val His Thr Ile Cys Asn Tyr Glu Gly

725	730	735
Ile Ser Val Gln Ile Lys His Ser Ser Pro Phe Ser Gly Val Val Phe		
740	745	750
Val Arg Asn Lys Tyr Asp Thr Cys Arg Val Lys Leu Lys Glu Arg Thr		
755	760	765
Ala Leu Phe Trp Phe Trp Gly Phe Gln Gln Ile Leu Glu Met Lys Pro		
770	775	780
Ile Ala Leu Ile Asn Ser Gln Lys His Gly Lys Gly Asn Lys Thr His		
785	790	795
Gly Asp Thr Leu Leu Ser Ile Glu Gly Ser Lys Lys Gln Ile Glu Gly		
805	810	815
Gly Ser Ser Thr Glu Asp Ile Gln Leu Ile Asn Ser Gln Lys Asp Leu		
820	825	830
Lys Arg Ser Arg Arg Gln Leu Gln Arg Asp Cys Gly Leu Gln Asp Met		
835	840	845
Asp Asn Gly Thr Tyr Lys Thr Val Ile Val Val Gln Thr Asn Asn Leu		
850	855	860
Gly Ile Pro Gly Leu Val Thr Ser Met Asp Gln Leu Tyr Glu Ile Ser		
865	870	875
Cys Asn Tyr Ser Ser Met Leu Gly Gly Lys Val Gln Thr Ala Ala Ala		
885	890	895
Leu Arg Val His Gly Pro Gln Pro Ser Leu Ile Gln Pro Arg Gly Lys		
900	905	910
Ile Glu Leu Gly Asn Pro Val Leu Met Gln Met Gly Pro Val Arg Ser		
915	920	925
Glu Arg Gln Ser Gly Glu Gly Pro Leu Ile Gln Ala Lys Leu Gly Asp		
930	935	940
Ile Leu Glu Leu Lys Trp Glu Ile Met Ala Met Asp Glu Glu Leu Asp		
945	950	955
Phe Leu Val Arg Asp Cys Phe Ala Glu Pro Gly Thr Ser Gly Asn Gln		
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Gly Glu Arg Leu Pro Leu Ile Glu Asn Gly Cys Pro Thr Pro Ala Val		
980	985	990
Ala Gln Lys Leu Ile Pro Asn Pro Ile Lys Ala Ile Asn Ser Ala Val		
995	1000	1005
Lys Leu Thr Tyr Leu Gln Ala Phe Arg Phe Asp Ser Ser Pro Ala Ile		
1010	1015	1020
Arg Ile Thr Cys His Leu Glu Leu Cys Lys Glu Asn Cys Lys Ser Val		
1025	1030	1035
Asn Cys Lys Phe Asn Asp Gly Ile Lys Glu Ser Trp Gly Arg Lys Arg		
1045	1050	1055
Arg Phe Ala Ile Asp Asn Asn Ile Asn Arg Lys Asn Glu Val Lys Glu		
1060	1065	1070
Phe Glu Thr Arg Arg Phe Val Val Pro Arg Phe Ala Gln Ala Thr Thr		
1075	1080	1085
Ser Leu Val Ile Val Asp Pro Leu Gln Gln Asn Ser Val Ile Lys		
1090	1095	1100
Thr Glu Gln Gln Gln Pro Phe Ile Ser His Ser Ser Ile Ser Lys		
1105	1110	1115
Gln Ile Phe Glu Asn Asn Lys Lys Glu Asn Asn Lys Asn Ile Thr Lys		
1125	1130	1135
Thr Ala Lys Lys Ser Ser Ser Leu Phe Glu Ala Phe Thr Glu Ala Ala		
1140	1145	1150
Gly Gly Arg Lys Ile Asn Leu Glu Leu Thr Thr Thr Asn Ser Glu Gln		
1155	1160	1165
Gln Gln Leu Cys Leu His Lys Trp Thr Leu Gly Gly Val Phe Gly Thr		
1170	1175	1180

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 Ile Asn Arg Phe Ile Val Gly Lys Arg Ile
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 <212> PRT
 <213> Heterodera glycines

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 35 40 45
 Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe Val Asp
 50 55 60
 Glu His Glu Asp Thr Val Ile Tyr Leu Asp Asn Asn Cys Ala Gly Cys
 65 70 75 80
 Glu Cys His Trp His Phe Asp Asn Phe Lys Thr Ser Gly Ile Leu Asn
 85 90 95
 Asp Gln Gln Phe Ala Ile Ala Ala Gln Cys Tyr Ala Pro Tyr Val Thr
 100 105 110
 Gln Tyr Val Ala Val Glu Gly Arg Gln Leu Ser Asp Glu Leu Asp His
 115 120 125
 Ser Phe Glu Gly Leu Glu Leu Ser Glu Cys Glu Leu Cys Thr Gln
 130 135 140
 Arg Leu Ser Val Thr Ala Asn Asp Phe Asn Cys Lys Ser Phe Met Tyr
 145 150 155 160
 Ser Asn Leu Thr Arg Ser Cys Val Leu Ser Asp Glu Arg Ser Arg Pro
 165 170 175
 Leu Gly Arg Ala Asn Leu Ala Glu Val Pro Gly Trp Thr Tyr Phe Glu
 180 185 190
 Ser Arg Gly Val Pro Ser Phe Thr Arg Val Pro Gln Met Leu Leu Val
 195 200 205
 Gly Phe Ala Ser Phe Val Met Glu Asn Val Pro Ser Val Thr Met Cys
 210 215 220
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 225 230 235 240
 Cys Lys Ser Val Met Tyr Tyr Tyr Asn Glu
 245 250

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 <212> PRT
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<400> 12

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 Glu Ile Pro Ser Tyr Pro Ala Cys Ser Asn Gly Glu Ser Pro Val Phe
 35 40 45
 Leu Leu Gln His Asn Ala Thr Ala Gly Asn Val Leu Lys Arg Ala Ser

50	55	60
Thr Ser His Leu Val Asp Cys Thr Asp Leu Cys Ser Ala Asn Asp Glu		
65	70	75
Cys Leu Ala Ile Thr Tyr Glu Asp Lys Glu Cys Lys Met Leu Ser Ser		80
85	90	95
Ile Gly Glu Ser Thr Gly His Leu Asn Asp Tyr Val Leu Leu Ser Lys		
100	105	110
Asn Cys Ala Lys Ser Ala Arg Ile Cys Ser Ser Pro Phe Gln Phe Asp		
115	120	125
Val His Arg Gln Lys Ile Leu Val Gly Phe Ala Arg Glu Val Val Ser		
130	135	140
Ala Asp Ser Leu Ser Leu Cys Leu Ser Ala Cys Leu Asn Ala Phe Asp		
145	150	155
Ser Phe Gly Phe Glu Cys Glu Ser Val Met Tyr Tyr Pro Val Asp Ser		160
165	170	175
Glu Cys Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe		
180	185	190
Gly Asp Glu Leu Asp Asp Asn Val Ile Tyr Leu Asp Asn Asn Cys Ala		
195	200	205
Gly Ser Gln Cys Tyr Ala Pro Tyr Ile Thr Gln Tyr Ile Ala Val Ala		
210	215	220
Asn Arg Gln Leu Ala Asn Glu Leu Asp Arg Gln Leu Ile Ala Asp Arg		
225	230	235
Glu Ser Cys Glu Ser Leu Cys Thr Gln Arg Leu Ser Thr Thr Asn		
245	250	255
Asp Phe Asn Cys Lys Ser Phe Met His Asn Pro Glu Thr Asn Val Cys		
260	265	270
Ile Leu Ser Asp Glu Arg Ser Lys Pro Leu Gly Arg Gly Asn Leu Val		
275	280	285
Lys Ala Asp Gly Phe Thr Tyr Tyr Glu Lys Lys Cys Phe Ala Ser Pro		
290	295	300
Arg Thr Cys Arg Asn Val Pro Ser Phe Glu Arg Ile Pro Gln Met Ile		
305	310	315
Leu Val Gly Phe Ala Ala Phe Val Met Glu Asn Val Pro Ser Val Thr		
325	330	335
Met Cys Leu Asp Gln Cys Thr Asn Pro Pro Pro Glu Thr Gly Glu Asn		
340	345	350
Phe Glu Cys Lys Ser Val Met Tyr Tyr Tyr Asn Glu Gln Glu Cys Ile		
355	360	365
Leu Asn Ala Glu Thr Arg Glu Asn Lys Ser Glu Leu Phe Ile Pro Glu		
370	375	380
Gly Glu Glu Phe Gln Val Asp Tyr Phe Asp Ile Thr Cys His Leu Arg		
385	390	395
Pro Glu Thr Cys Pro Asn Gly Thr Thr Leu His Thr Val Arg Thr Val		
405	410	415
Asn Ala Ala Leu Pro Glu Gly Glu Gly Ser Ile His Ile Leu Gln Ser		
420	425	430
Ala Gly Asn Ser Val Ala Asp Cys Met Thr Lys Cys Tyr Glu Met Ala		
435	440	445
Pro Glu Lys Cys Arg Ala Phe Asn Phe Asp Lys Gln Thr Ser Asp Cys		
450	455	460
Asp Leu Leu Tyr Val Asp Gly Lys Thr Thr Leu Arg Pro Ala Val His		
465	470	475
Ser Gly Ile Asp Leu Tyr Asp Leu His Cys Leu Glu Gln Thr Lys Val		
485	490	495
Cys Ala Gln Lys Asn Asn Val Thr Arg Phe Ser Arg Tyr Leu Tyr Ser		
500	505	510

Ile Tyr Asp Ala Val Pro Ser Gln Phe Tyr Glu Ala Thr Ala Leu Thr
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 Asn Cys Leu Asn Leu Cys Ala Tyr Thr Glu Arg Cys Glu Gly Val Asn
 530 535 540
 Tyr Asn Arg Arg Asn Gly Arg Cys Glu Leu Phe Asp Lys Val Glu Gly
 545 550 555 560
 Asn Gly Lys Pro Ser Asp Phe Thr Asp Phe Tyr Lys Asn Leu Cys Leu
 565 570 575
 Val Glu Glu Val Glu Ser Glu Tyr Ser Ala Ala Ala Asn Val Pro Lys
 580 585 590
 His Leu Leu Pro Asn Val Ser His Ser Ala Val Thr Gln Lys Gln Glu
 595 600 605
 Ala Lys Leu His Ile Ile Ser Ala Lys Thr Lys Pro Phe Leu Arg Glu
 610 615 620
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 625 630 635 640
 Ser Ala Ser Gly Lys Val Ser Gly Glu Ala Gly Ser Ser Thr Thr Phe
 645 650 655
 Ser Ile Ser Ser Gly Arg Leu Pro Gly Pro Val Val Gln Ile Ala
 660 665 670
 Pro Asn Ala Val Gln Thr Val Cys Asn Tyr Glu Gly Ile Lys Val Gln
 675 680 685
 Met Glu Asn Pro Lys Ala Phe Ser Gly Val Ile Phe Val Lys Asn Arg
 690 695 700
 Tyr Glu Thr Cys Arg Val Glu Val Thr Asp Ser Glu Ser Ala Pro Leu
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 Val Ile Gly Leu Pro Pro Asn Phe Gly Ser Lys Met Val Ala Asp Glu
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 Lys Val Ala Ala Ser Glu Ala Asn Ile Gln Pro Glu Ile Ser Gly Gly
 740 745 750
 Asp Lys Leu Asp Lys Pro Ala Asp Glu Leu Arg Ile Arg Arg Gln Ala
 755 760 765
 Leu Glu Leu His Arg Asp Cys Gly Ile Gln Asp Met Asn Asn Gly Thr
 770 775 780
 Tyr Lys Ser Thr Val Val Gln Thr Asn Asn Leu Gly Ile Pro Gly
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 805 810 815
 Ser Met Leu Gly Gly Lys Val Thr Ala Gly Ala Asn Leu Thr Ile Asp
 820 825 830
 Gly Pro Glu Ala Ser Leu Ile Gln Pro Arg Gly Lys Ile Glu Leu Gly
 835 840 845
 Asn Pro Val Leu Met Gln Met Leu Ser Gly Gln Gly Glu Pro Val Leu
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 120

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cctgaaacat	gtccaaatgg	cacaacatta	catactgtac	gtacggtaa	tgcagcactc	1260
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atgacaaaat	gttacgagat	ggctcccgag	aatgtcg	cattcaattt	tgcataacgt	1380
acatctgact	gtgacctgct	gtacgttgc	ggaaagacaa	ctttacgacc	agcagtccac	1440
tcgggcattt	atctctacga	ccttcattgc	ctagagcaga	aaaagtttgc	cgctcagaaa	1500
aacaacgtaa	cacgatttc	gagatatttgc	tacagtat	atgtatgcgt	gccatcgca	1560
ttctacgaag	caactgcct	cacaatttgc	cttaatctt	gccccatatac	cgagcgttgc	1620
gaaggtgtaa	attacaacag	aaggaatgg	cgttgcata	tatttgataa	gtcgaagga	1680

aatggaaagc	caagtgattt	cacggatttt	tacaaaatc	tttgtctgg	ggaagaagta	1740
gaatcagaat	atagccgc	agctaattgt	cccaaacatc	tccttccgaa	tgttcacat	1800
tctcaggtt	ctcagaaaca	agaagctaaa	ttacacatta	tctcagcaaa	aacaaagcct	1860
ttccctacg	aacaggaagc	acacgcacga	gctccagaaa	caataacagc	gaagtcgtct	1920
tca	gaaaagtaag	tgttgaagca	ggatcatcaa	ctacattcag	catttctca	1980
tccggaggc	ttccaggg	cc	attgctccaa	atgcagtgc	aacagttgc	2040
aattatgaag	gcatcaa	agt	gcagatggag	aacccaaag	cctttcggg	2100
gttaaaaata	ggtatgaa	ac	ctgtcgagta	gagg	tacgg	2160
gttaattgg	taccac	ggaa	tttgg	ctgatgaaa	ggttgcgc	2220
agcgaagc	atattcaacc	agaaatatcc	ggaggcaca	aactggataa	acccgcgtat	2280
gaactgc	taagacgaca	ac	ctacacagag	attgcgg	atccaggatatg	2340
aacaatgg	cttataaaatc	aacgg	gtacaaacaa	ataacttgg	tataactgg	2400
ctgtaactt	ccatggatca	gat	tttgg	attatagttc	aatgc	2460
ggaaaagtt	ctgctgg	tc	caatctcaca	attgatgg	tcttattca	2520
ccccgaggaa	aaatcgaact	tgtaa	cccg	tgcttatgc	agatgtt	2580
gaacctgtcc	tacaagc	aaa	actaggtgac	attctgc	ac	2640
atg						2643

<210> 16

<211> 1065

<212> PRT

<213> *Caenorhabditis elegans*

<400> 16

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Asp	Thr	Leu	Pro	Ser	Val	Thr	Leu	Cys	Pro	Pro	Glu	Thr	Gln	Thr	Ile
						20			25						30
Phe	Val	Leu	Gln	His	Asn	Thr	Thr	Val	Gly	Ala	Arg	Ile	Arg	Thr	Ile
						35			40						45
Pro	Thr	Ser	Asn	Leu	Ala	Glu	Cys	Ser	Asp	His	Cys	Ser	Ala	Ser	Leu
						50			55						60
Asp	Cys	Gln	Gly	Val	Glu	Phe	Lys	Asp	Gly	Ser	Cys	Ala	Val	Phe	Arg
						65			70						80
Ala	Gly	Ser	Glu	Lys	Ala	Thr	Ala	Gly	Ser	Gln	Leu	Leu	Thr	Lys	Thr
						85			90						95
Cys	Val	Lys	Ser	Asp	Arg	Val	Cys	Gln	Ser	Pro	Phe	Gln	Phe	Asp	Leu
						100			105						110
Phe	Glu	Gln	Arg	Ile	Leu	Val	Gly	Phe	Ala	Arg	Glu	Val	Val	Pro	Ala
						115			120						125
Ala	Asn	Ile	Gln	Ile	Cys	Met	Ala	Ala	Cys	Leu	Asn	Ala	Phe	Asp	Thr
						130			135						140
Phe	Gly	Phe	Glu	Cys	Glu	Ser	Ala	Met	Phe	Tyr	Pro	Val	Asp	Gln	Glu
						145			150						160
Cys	Ile	Leu	Asn	Thr	Glu	Asp	Arg	Leu	Asp	Arg	Pro	Ser	Leu	Phe	Val
						165			170						175
Glu	Glu	Ser	Asp	Asp	Thr	Val	Ile	Tyr	Met	Asp	Asn	Asn	Cys	Ala	Gly
						180			185						190
Phe	Pro	Leu	Val	Phe	Lys	Asn	Tyr	Asn	Tyr	Gln	Lys	Thr	Thr	Phe	Ser
						195			200						205
Lys	Ser	Gln	Cys	Tyr	Pro	Pro	Tyr	Ile	Thr	Gln	Tyr	Ile	Ala	Val	Glu
						210			215						220
Gly	Lys	Gln	Leu	Lys	Asn	Glu	Leu	Asp	Arg	Ile	Ile	Asn	Val	Asp	Leu
						225			230						240
Asp	Ser	Cys	Gln	Ala	Leu	Cys	Thr	Gln	Arg	Leu	Ser	Ile	Ser	Ser	Asn
						245			250						255
Asp	Phe	Asn	Cys	Lys	Ser	Phe	Met	Tyr	Asn	Asn	Lys	Thr	Arg	Thr	Cys

260	265	270
Ile Leu Ala Asp Glu Arg Ser Lys Pro Leu Gly Arg Ala Asp Leu Ile		
275	280	285
Ala Thr Glu Gly Phe Thr Tyr Phe Glu Lys Lys Cys Phe Ala Ser Pro		
290	295	300
Asn Thr Cys Arg Asn Val Pro Ser Phe Lys Arg Val Pro Gln Met Ile		
305	310	315
Leu Val Gly Phe Ala Ala Phe Val Met Glu Asn Val Pro Ser Val Thr		
325	330	335
Met Cys Leu Asp Gln Cys Thr Asn Pro Pro Pro Glu Thr Gly Asp Gly		
340	345	350
Phe Val Cys Lys Ser Val Met Tyr Tyr Asn Glu Gln Glu Cys Ile		
355	360	365
Leu Asn Ser Glu Thr Arg Glu Ser Lys Pro Glu Leu Phe Ile Pro Glu		
370	375	380
Gly Glu Glu Phe Leu Val Asp Tyr Phe Asp Ile Thr Cys His Leu Lys		
385	390	395
Gln Glu Lys Cys Pro Thr Gly Gln His Leu Lys Ala Ile Arg Thr Ile		
405	410	415
Asn Ala Ala Leu Pro Glu Gly Glu Ser Glu Leu His Val Leu Lys Ala		
420	425	430
Ser Ala Ala Lys Gly Ile Lys Glu Cys Val Ala Lys Cys Phe Gly Leu		
435	440	445
Ala Pro Glu Lys Cys Arg Ser Phe Asn Tyr Asp Lys Lys Thr Lys Ser		
450	455	460
Cys Asp Leu Leu Tyr Leu Asp Gly His Asn Thr Leu Gln Pro Gln Val		
465	470	475
Arg Gln Gly Val Asp Leu Tyr Asp Leu His Cys Leu Ala Val Glu Asn		
485	490	495
Asp Cys Ser Ala Asn Lys Asp Asp Ala Leu Phe Ser Arg Tyr Leu His		
500	505	510
Thr Lys Gln Arg Gly Ile Pro Ala Lys Val Tyr Lys Val Val Ser Leu		
515	520	525
Asn Ser Cys Leu Glu Val Cys Ala Gly Asn Pro Thr Cys Ala Gly Ala		
530	535	540
Asn Tyr Asn Arg Arg Leu Gly Asp Cys Thr Leu Phe Asp Ala Ile Asp		
545	550	555
Asp Asp Ala Glu Ile Asn Glu His Thr Asp Phe Tyr Lys Asn Leu Cys		
565	570	575
Val Thr Lys Glu Ile Asp Thr Gly Ala Ser Ala Ala Asn Val Pro		
580	585	590
Glu Thr Lys His Arg Val Ser Gly Thr Val Val Glu Gly Lys Asp Ser		
595	600	605
Lys Ser Gln Leu Leu Ala Thr Lys Lys Val Lys Lys Pro Thr Ile Lys		
610	615	620
Asn Thr Glu His Arg Arg Ala Pro Glu Ser Thr Val Pro Ile Gly Pro		
625	630	635
Pro Val Glu Val Lys Ala Glu Ala Ile Gln Thr Ile Cys Asn Tyr Glu		
645	650	655
Gly Ile Lys Val Gln Ile Asn Asn Gly Glu Pro Phe Ser Gly Val Ile		
660	665	670
Phe Val Lys Asn Lys Phe Asp Thr Cys Arg Val Glu Val Ala Asn Ser		
675	680	685
Asn Ala Ala Thr Leu Val Leu Gly Leu Pro Lys Asp Phe Gly Met Arg		
690	695	700
Pro Ile Ser Leu Asp Asn Ile Asp Asp Asn Glu Thr Gly Lys Asn Lys		
705	710	720

Thr Lys Lys Gly Glu Glu Thr Pro Leu Lys Asp Glu Ile Glu Glu Phe
 725 730 735
 Arg Gln Lys Arg Gln Ala Ala Glu Phe Arg Asp Cys Gly Leu Val Asp
 740 745 750
 Leu Leu Asn Gly Thr Tyr Lys Ser Thr Val Val Ile Gln Thr Asn Asn
 755 760 765
 Leu Gly Ile Pro Gly Leu Val Thr Ser Met Asp Gln Leu Tyr Glu Val
 770 775 780
 Ser Cys Asp Tyr Ser Ser Met Leu Gly Gly Arg Val Gln Ala Gly Tyr
 785 790 795 800
 Asn Met Thr Val Thr Gly Pro Glu Ala Asn Leu Ile Gln Pro Arg Gly
 805 810 815
 Lys Ile Glu Leu Gly Asn Pro Val Leu Met Gln Leu Leu Asn Gly Asp
 820 825 830
 Gly Thr Glu Gln Pro Leu Val Gln Ala Lys Leu Gly Asp Ile Leu Glu
 835 840 845
 Leu Arg Trp Glu Ile Met Ala Met Asp Asp Glu Leu Asp Phe Phe Val
 850 855 860
 Lys Asn Cys His Ala Glu Pro Gly Val Ala Gly Gly Lys Ala Gly Ala
 865 870 875 880
 Gly Glu Lys Leu Arg Leu Ile Asp Gly Gly Cys Pro Thr Pro Ala Val
 885 890 895
 Ala Gln Lys Leu Ile Pro Gly Ala Ile Glu Ile Lys Ser Ser Ala Val
 900 905 910
 Lys Thr Thr Lys Met Gln Ala Phe Arg Phe Asp Ser Ser Ala Ser Ile
 915 920 925
 Arg Val Thr Cys Glu Val Glu Ile Cys Lys Gly Asp Cys Glu Pro Val
 930 935 940
 Glu Cys Ala Leu Thr Gly Gly Val Lys Lys Ser Phe Gly Arg Lys Lys
 945 950 955 960
 Arg Glu Val Ser Asn Asn Ile Glu Glu Phe Glu Thr Asn Arg Tyr Leu
 965 970 975
 Ile Pro Arg Arg Ser His Ala Thr Thr Ser Ile Val Ile Ile Asp Pro
 980 985 990
 Leu Gln Gln Val Asn Glu Pro Val Ala Met Ser Arg Ala Ser Thr Leu
 995 1000 1005
 Asp Leu Leu Arg Glu Asp Ala His Glu Val Gln Met Ile Glu Glu Gly
 1010 1015 1020
 Ser Ile Cys Leu Asn Ser Val Thr Val Phe Ala Ile Phe Gly Thr Leu
 1025 1030 1035 1040
 Ala Val Leu Ile Leu Gly Gln Thr Val Val Ile Ala His Tyr Ala Val
 1045 1050 1055
 Arg Arg Phe Ser Ser Glu Lys Thr Ala
 1060 1065

<210> 17
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 <212> PRT
 <213> *Caenorhabditis elegans*

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 Asp Thr Leu Pro Ser Val Thr Leu Cys Pro Pro Glu Thr Gln Thr Ile
 20 25 30
 Phe Val Leu Gln His Asn Thr Thr Val Gly Ala Arg Ile Arg Thr Ile
 35 40 45

Pro Thr Ser Asn Leu Ala Glu Cys Ser Asp His Cys Ser Ala Ser Leu
 50 55 60
 Asp Cys Gln Gly Val Glu Phe Lys Asp Gly Ser Cys Ala Val Phe Arg
 65 70 75 80
 Ala Gly Ser Glu Lys Ala Thr Ala Gly Ser Gln Leu Leu Thr Lys Thr
 85 90 95
 Cys Val Lys Ser Asp Arg Val Cys Gln Ser Pro Phe Gln Phe Asp Leu
 100 105 110
 Phe Glu Gln Arg Ile Leu Val Gly Phe Ala Arg Glu Val Val Pro Ala
 115 120 125
 Ala Asn Ile Gln Ile Cys Met Ala Ala Cys Leu Asn Ala Phe Asp Thr
 130 135 140
 Phe Gly Phe Glu Cys Glu Ser Ala Met Phe Tyr Pro Val Asp Gln Glu
 145 150 155 160
 Cys Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Ser Leu Phe Val
 165 170 175
 Glu Glu Ser Asp Asp Thr Val Ile Tyr Met Asp Asn Asn Cys Ala Gly
 180 185 190
 Phe Pro Leu Val Phe Lys Asn Tyr Asn Tyr Gln Lys Thr Thr Phe Ser
 195 200 205
 Lys Ser Gln Cys Tyr Pro Pro Tyr Ile Thr Gln Tyr Ile Ala Val Glu
 210 215 220
 Gly Lys Gln Leu Lys Asn Glu Leu Asp Arg Ile Ile Asn Val Asp Leu
 225 230 235 240
 Asp Ser Cys Gln Ala Leu Cys Thr Gln Arg Leu Ser Ile Ser Ser Asn
 245 250 255
 Asp Phe Asn Cys Lys Ser Phe Met Tyr Asn Asn Lys Thr Arg Thr Cys
 260 265 270
 Ile Leu Ala Asp Glu Arg Ser Lys Pro Leu Gly Arg Ala Asp Leu Ile
 275 280 285
 Ala Thr Glu Gly Phe Thr Tyr Phe Glu Lys Lys Cys Phe Ala Ser Pro
 290 295 300
 Asn Thr Cys Arg Asn Val Pro Ser Phe Lys Arg Val Pro Gln Met Ile
 305 310 315 320
 Leu Val Gly Phe Ala Ala Phe Val Met Glu Asn Val Pro Ser Val Thr
 325 330 335
 Met Cys Leu Asp Gln Cys Thr Asn Pro Pro Pro Glu Thr Gly Asp Gly
 340 345 350
 Phe Val Cys Lys Ser Val Met Tyr Tyr Tyr Asn Glu Gln Glu Cys Ile
 355 360 365
 Leu Asn Ser Glu Thr Arg Glu Ser Lys Pro Glu Leu Phe Ile Pro Glu
 370 375 380
 Gly Glu Glu Phe Leu Val Asp Tyr Phe Asp Ile Thr Cys His Leu Lys
 385 390 395 400
 Gln Glu Lys Cys Pro Thr Gly Gln His Leu Lys Ala Ile Arg Thr Ile
 405 410 415
 Asn Ala Ala Leu Pro Glu Gly Glu Ser Glu Leu His Val Leu Lys Ala
 420 425 430
 Ser Ala Ala Lys Gly Ile Lys Glu Cys Val Ala Lys Cys Phe Gly Leu
 435 440 445
 Ala Pro Glu Lys Cys Arg Ser Phe Asn Tyr Asp Lys Lys Thr Lys Ser
 450 455 460
 Cys Asp Leu Leu Tyr Leu Asp Gly His Asn Thr Leu Gln Pro Gln Val
 465 470 475 480
 Arg Gln Gly Val Asp Leu Tyr Asp Leu His Cys Leu Ala Ala Met Pro
 485 490 495
 Leu Val Glu Asn Asp Cys Ser Ala Asn Lys Asp Asp Ala Leu Phe Ser

500	505	510
Arg Tyr Leu His Thr Lys Gln Arg Gly Ile Pro Ala Lys Val Tyr Lys		
515	520	525
Val Val Ser Leu Asn Ser Cys Leu Glu Val Cys Ala Gly Asn Pro Thr		
530	535	540
Cys Ala Gly Ala Asn Tyr Asn Arg Arg Leu Gly Asp Cys Thr Leu Phe		
545	550	555
Asp Ala Ile Asp Asp Asp Ala Glu Ile Asn Glu His Thr Asp Phe Tyr		
565	570	575
Lys Asn Leu Cys Val Thr Lys Glu Ile Asp Thr Gly Ala Ser Ala Ala		
580	585	590
Ala Asn Val Pro Glu Thr Lys His Arg Val Ser Gly Thr Val Val Glu		
595	600	605
Gly Lys Asp Ser Lys Ser Gln Leu Leu Ala Thr Lys Lys Val Lys Lys		
610	615	620
Pro Thr Ile Lys Asn Thr Glu His Arg Arg Ala Pro Glu Ser Thr Val		
625	630	635
640		
Pro Ile Gly Pro Pro Val Glu Val Lys Ala Glu Ala Ile Gln Thr Ile		
645	650	655
Cys Asn Tyr Glu Gly Ile Lys Val Gln Ile Asn Asn Gly Glu Pro Phe		
660	665	670
Ser Gly Val Ile Phe Val Lys Asn Lys Phe Asp Thr Cys Arg Val Glu		
675	680	685
Val Ala Asn Ser Asn Ala Ala Thr Leu Val Leu Gly Leu Pro Lys Asp		
690	695	700
Phe Gly Met Arg Pro Ile Ser Leu Asp Asn Ile Asp Asp Asn Glu Thr		
705	710	715
720		
Gly Lys Asn Lys Thr Lys Gly Glu Glu Thr Pro Leu Lys Asp Glu		
725	730	735
Ile Glu Glu Phe Arg Gln Lys Arg Gln Ala Ala Glu Phe Arg Asp Cys		
740	745	750
Gly Leu Val Asp Leu Leu Asn Gly Thr Tyr Lys Ser Thr Val Val Ile		
755	760	765
Gln Thr Asn Asn Leu Gly Ile Pro Gly Leu Val Thr Ser Met Asp Gln		
770	775	780
Leu Tyr Glu Val Ser Cys Asp Tyr Ser Ser Met Leu Gly Gly Arg Val		
785	790	795
800		
Gln Ala Gly Tyr Asn Met Thr Val Thr Gly Pro Glu Ala Asn Leu Ile		
805	810	815
Gln Pro Arg Gly Lys Ile Glu Leu Gly Asn Pro Val Leu Met Gln Leu		
820	825	830
Leu Asn Gly Asp Gly Thr Glu Gln Pro Leu Val Gln Ala Lys Leu Gly		
835	840	845
Asp Ile Leu Glu Leu Arg Trp Glu Ile Met Ala Met Asp Asp Glu Leu		
850	855	860
Asp Phe Phe Val Lys Asn Cys His Ala Glu Pro Gly Val Ala Gly Gly		
865	870	875
880		
Lys Ala Gly Ala Gly Glu Lys Leu Arg Leu Ile Asp Gly Gly Cys Pro		
885	890	895
Thr Pro Ala Val Ala Gln Lys Leu Ile Pro Gly Ala Ile Glu Ile Lys		
900	905	910
Ser Ser Ala Val Lys Thr Thr Lys Met Gln Ala Phe Arg Phe Asp Ser		
915	920	925
Ser Ala Ser Ile Arg Val Thr Cys Glu Val Glu Ile Cys Lys Gly Asp		
930	935	940
Cys Glu Pro Val Glu Cys Ala Leu Thr Gly Gly Val Lys Lys Ser Phe		
945	950	955
960		

Gly Arg Lys Lys Arg Glu Val Ser Asn Asn Ile Glu Glu Phe Glu Thr
 965 970 975
 Asn Arg Tyr Leu Ile Pro Arg Arg Ser His Ala Thr Thr Ser Ile Val
 980 985 990
 Ile Ile Asp Pro Leu Gln Gln Val Asn Glu Pro Val Ala Met Ser Arg
 995 1000 1005
 Ala Ser Thr Leu Asp Leu Leu Arg Glu Asp Ala His Glu Val Gln Met
 1010 1015 1020
 Ile Glu Glu Gly Ser Ile Cys Leu Asn Ser Val Thr Val Phe Ala Ile
 1025 1030 1035 1040
 Phe Gly Thr Leu Ala Val Leu Ile Leu Gly Gln Thr Val Val Ile Ala
 1045 1050 1055
 His Tyr Ala Val Arg Arg Phe Ser Ser Glu Lys Thr Ala
 1060 1065

<210> 18
 <211> 741
 <212> PRT
 <213> *Caenorhabditis elegans*

<400> 18
 Met Trp Gly Val Ile Phe Leu Leu Leu Ser Ile Val Pro Ala Ala Gln
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 Ser Val Phe Glu Cys Ser Ser His Glu Thr Thr Ala Phe Val Arg Ile
 20 25 30
 Pro Arg Ala Arg Leu Asp Gly Thr Pro Val Val Ile Ser Thr Ala Gly
 35 40 45
 His Asp Leu Thr Cys Ala Gln Tyr Cys Arg Asn Asn Ile Glu Pro Thr
 50 55 60
 Thr Gly Ala Gln Arg Val Cys Ala Ser Phe Asn Phe Asp Gly Arg Glu
 65 70 75 80
 Thr Cys Tyr Phe Phe Asp Asp Ala Ala Thr Pro Ala Gly Thr Ser Gln
 85 90 95
 Leu Thr Ala Asn Pro Ser Ala Asn Asn Phe Tyr Tyr Glu Lys Thr Cys
 100 105 110
 Ile Pro Asn Val Ser Ala His Glu Ala Cys Thr Tyr Arg Ser Phe Ser
 115 120 125
 Phe Glu Arg Ala Arg Asn Thr Gln Leu Glu Gly Phe Val Lys Lys Ser
 130 135 140
 Val Thr Val Glu Asn Arg Glu His Cys Leu Ser Ala Cys Leu Lys Glu
 145 150 155 160
 Lys Glu Phe Val Cys Lys Ser Val Asn Phe His Tyr Asp Thr Ser Leu
 165 170 175
 Cys Glu Leu Ser Val Glu Asp Lys Arg Ser Lys Pro Thr His Val Arg
 180 185 190
 Met Ser Glu Lys Ile Asp Tyr Tyr Asp Asn Asn Cys Leu Ser Arg Gln
 195 200 205
 Asn Arg Cys Gly Pro Ser Gly Gly Asn Leu Val Phe Val Lys Thr Thr
 210 215 220
 Asn Phe Glu Ile Arg Tyr Tyr Asp His Thr Gln Ser Val Glu Ala Gln
 225 230 235 240
 Glu Ser Tyr Cys Leu Gln Lys Cys Leu Asp Ser Leu Asn Thr Phe Cys
 245 250 255
 Arg Ser Val Glu Phe Asn Pro Lys Glu Lys Asn Cys Ile Val Ser Asp
 260 265 270
 Glu Asp Thr Phe Ser Arg Ala Asp Gln Gln Gly Gln Val Val Gly Lys
 275 280 285

Asp Tyr Tyr Glu Pro Ile Cys Val Ala Ala Asp Leu Ser Ser Ser Thr
 290 295 300
 Cys Arg Gln Gln Ala Ala Phe Glu Arg Phe Ile Gly Ser Ser Ile Glu
 305 310 315 320
 Gly Glu Val Val Ala Ser Ala Gln Gly Val Thr Ile Ser Asp Cys Ile
 325 330 335
 Ser Leu Cys Phe Gln Asn Leu Asn Cys Lys Ser Ile Asn Tyr Asp Arg
 340 345 350
 Thr Ala Ser Ser Cys Phe Ile Tyr Ala Val Gly Arg Gln Asp Ala Asn
 355 360 365
 Ile Lys Ala Asn Pro Ser Met Asp Tyr Tyr Glu Phe Asn Cys Glu Ser
 370 375 380
 Gln Phe Gly Gly Met Ala Leu Cys Thr Asn Glu Gly Ile Arg Phe Ile
 385 390 395 400
 Val Asn Thr Lys Glu Pro Tyr Thr Gly Ala Ile Tyr Ala Ala Glu Arg
 405 410 415
 Phe Ser Thr Cys Ser Gln Val Val Glu Asn Ala Lys Gln Ile Ser Ile
 420 425 430
 Thr Phe Pro Pro Pro Thr Val Ser Ser Asp Cys Gly Thr Val Ile Arg
 435 440 445
 Asp Gly Lys Met Glu Ala Leu Val Val Val Ser Leu Asp Gly Val Leu
 450 455 460
 Pro His Gln Val Thr Thr Glu Trp Asp Arg Phe Tyr Arg Val Ser Cys
 465 470 475 480
 Asp Val Ser Met Asp Lys Met Val Lys Glu Gly Ser Val Val Val Thr
 485 490 495
 Thr Ile Tyr Glu Ala Ser Ser Gln Asn Thr Thr Val Leu Asp Val Ala
 500 505 510
 Thr Pro Pro Pro Val Ser Ala Glu Leu Gln Ile Leu Asn Gln Leu Glu
 515 520 525
 Glu Pro Leu His Lys Ala Ser Ile Gly Asp Pro Leu Leu Leu Val Ile
 530 535 540
 Thr Ser Glu Gln Ala Gly Pro His Asn Met Met Val Thr Glu Cys Thr
 545 550 555 560
 Ala Thr Arg Val Gly Gly Phe Gly Asp Thr Val Pro Phe Thr Leu Ile
 565 570 575
 Glu Asn Gly Cys Pro Arg Tyr Pro Ala Leu Val Gly Pro Val Glu Gln
 580 585 590
 Asp Phe Asp Lys Asn Arg Leu Lys Ser Asp Leu Arg Ala Phe Arg Leu
 595 600 605
 Asp Gly Ser Tyr Asp Val Gln Ile Val Cys Ser Ile Met Phe Cys Ala
 610 615 620
 Gly Pro Asn Gly Cys Pro Val Ser Asn Cys Leu Asp Ser Gly Thr Asn
 625 630 635 640
 Glu Leu Phe Met Ser His Gly Arg Lys Lys Arg Ser Ala Asp Leu Glu
 645 650 655
 Ala Gly Glu Thr Glu Glu Lys Leu Ser Ala Ile Ile Arg Val Phe Ala
 660 665 670
 Lys Gly Glu Asp Glu Glu Glu Met Glu Met Ala Asn Asn Thr Met Met
 675 680 685
 Thr Ser Met Ser Asp Ser Thr Glu Leu Leu Cys Ile Ala Glu Pro Phe
 690 695 700
 Phe Val Ser Ser Val Val Ser Leu Ser Val Leu Cys Phe Ala Leu Ser
 705 710 715 720
 Ala Ile Ile Ala Ile Trp Gly Cys His Ser Leu His Ser Lys Pro Val
 725 730 735
 Lys Gln Val Ala Ala

740

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<400> 19		
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cgacuggagc acgaggacac ugacauggac ugaaggagua gaaa	44	
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ggacactgac atggactgaa ggagta		26
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tgacagatgg aacattctcc		20
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acttcaggac acgacttgac		20
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cgtttagac agtcgctgag tacata		26
<210> 32		
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ccaactcggtt agctagctga cg		22
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cgaacatgtc gcaatgtac		19
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ttyggnttyg artgygar		18
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gatcgaggca catcgttac		19
<210> 37		
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gttagatgc tgttgatac		19
<210> 38		
<211> 20		
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<222> 9, 15
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<400> 38
tcdatyttnc cyctnggytg 20

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 39
caagatatgg acaatggaac 20

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 40
atacattcgg catccaatgg 20

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 41
actgactcgc attcaaagcc 20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
tagctaatct agcttagtgtc 20

<210> 43
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
 <222> 15
 <223> n = a, t, c, or g

 <400> 43
 garcaraara tgctngt
 17

 <210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 44
 tgytcrttrt artartacat
 20

 <210> 45
 <211> 1068
 <212> PRT
 <213> *Caenorhabditis briggsae*

 <400> 45
 Met Lys Val Phe Ala Val Val Ala Leu Leu Ala Val Ser Ala Leu Ala
 1 5 10 15
 Asp Thr Leu Pro Ser Val Thr Ile Cys Pro Pro Glu Thr Gln Thr Ile
 20 25 30
 Phe Val Leu Gln His Asn Ser Thr Val Gly Ala Arg Ile Arg Thr Ile
 35 40 45
 Pro Thr Ser Asn Leu Ala Glu Cys Ser Asp His Cys Ala Ala Ser Leu
 50 55 60
 Asp Cys Gln Gly Val Glu Phe Lys Asp Gly Ser Cys Ala Val Phe Arg
 65 70 75 80
 Ala Gly Ser Glu Lys Ala Thr Lys Gly Ser Gln Leu Leu Thr Lys Ser
 85 90 95
 Cys Val Lys Ser Asp Arg Val Cys Gln Ser Pro Phe Gln Phe Asp Leu
 100 105 110
 Phe Glu Gln Lys Ile Leu Val Gly Phe Ala Arg Glu Val Val Pro Ala
 115 120 125
 Glu Asn Ile Gln Val Cys Met Ala Ala Cys Leu Asn Ala Phe Asp Thr
 130 135 140
 Phe Gly Phe Glu Cys Glu Ser Ala Met Phe Tyr Pro Val Asp Gln Glu
 145 150 155 160
 Cys Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Ser Leu Phe Val
 165 170 175
 Asp Glu Ala Asp Asp Thr Val Ile Tyr Met Asp Asn Asn Cys Ala Gly
 180 185 190
 Cys Lys Phe Gln Asn Pro Cys Ser His Val Asp Leu Tyr Phe Ser Leu
 195 200 205
 Ala Gln Cys Tyr Pro Pro Tyr Ile Thr Gln Tyr Ile Ala Val Glu Gly
 210 215 220
 Lys Gln Leu Lys Asn Glu Leu Asp Arg Ile Ile Asn Val Asp Leu Asp
 225 230 235 240
 Ser Cys Gln Ala Leu Cys Thr Gln Arg Leu Ser Ile Ser Ser Asn Asp
 245 250 255

Phe Asn Cys Lys Ser Phe Met Tyr Asn Asn Lys Thr Arg Thr Cys Ile
 260 265 270
 Leu Ala Asp Glu Arg Ser Lys Pro Leu Gly Arg Ala Asp Leu Val Ala
 275 280 285
 Thr Glu Gly Phe Thr Tyr Phe Glu Lys Lys Cys Phe Ala Ser Pro Asn
 290 295 300
 Thr Cys Arg Asn Val Pro Ser Phe Lys Arg Val Pro Gln Met Ile Leu
 305 310 315 320
 Val Gly Phe Ala Ala Phe Val Met Glu Asn Val Pro Ser Val Thr Met
 325 330 335
 Cys Leu Asp Gln Cys Thr Asn Pro Pro Pro Glu Thr Gly Asp Gly Phe
 340 345 350
 Val Cys Lys Ser Val Met Tyr Tyr Asn Glu Gln Glu Cys Ile Leu
 355 360 365
 Asn Ser Glu Thr Arg Glu Ser Lys Pro Glu Leu Phe Ile Pro Glu Gly
 370 375 380
 Glu Glu Phe Leu Val Asp Tyr Phe Asp Ile Thr Cys His Leu Lys Gln
 385 390 395 400
 Glu Lys Cys Pro Ala Gly Gln His Leu Lys Ala Ile Arg Thr Ile Asn
 405 410 415
 Ala Ala Leu Pro Glu Gly Glu Ser Glu Leu His Val Leu Lys Ser Ser
 420 425 430
 Ala Ala Lys Gly Ile Lys Glu Cys Val Ala Lys Cys Phe Gly Leu Ala
 435 440 445
 Pro Glu Lys Cys Arg Ser Phe Asn Tyr Asp Lys Lys Thr Lys Ser Cys
 450 455 460
 Asp Leu Leu Tyr Leu Asp Gly His Asn Thr Leu Gln Pro Gln Val Arg
 465 470 475 480
 Gln Gly Val Asp Leu Tyr Asp Leu His Cys Leu Ala Ala Leu Pro Leu
 485 490 495
 Val Glu Asn Asp Cys Ser Ala Asn Lys Asp Asp Ala Leu Phe Ser Arg
 500 505 510
 Tyr Leu His Thr Lys Gln Arg Gly Ile Pro Ala Lys Ser Tyr Lys Val
 515 520 525
 Val Ser Leu Asn Ser Cys Leu Glu Val Cys Ala Gly Asn Pro Thr Cys
 530 535 540
 Ala Gly Ala Asn Tyr Asn Arg Arg Leu Gly Asp Cys Ser Leu Phe Asp
 545 550 555 560
 Ala Ile Asp Lys Asp Ala Glu Val Asn Glu His Thr Asp Phe Tyr Lys
 565 570 575
 Asn Leu Cys Val Thr Lys Glu Val Asp Thr Gly Ala Ser Ala Ala Ala
 580 585 590
 Asn Val Pro Glu Thr Lys His Arg Val Ser Gly Thr Val Val Glu Gly
 595 600 605
 Lys Asp Ser Lys Ala Gln Leu Leu Ala Thr Lys Lys Val Lys Lys Pro
 610 615 620
 Thr Ile Lys Asn Thr Glu His Arg Arg Ala Pro Glu Ser Thr Val Pro
 625 630 635 640
 Leu Gly Pro Pro Val Glu Val Lys Ala Glu Ala Ile Gln Thr Ile Cys
 645 650 655
 Asn Tyr Glu Gly Ile Lys Val Gln Ile Asn Asn Gly Glu Pro Phe Ser
 660 665 670
 Gly Val Ile Phe Val Lys Asn Lys Phe Asp Thr Cys Arg Val Glu Val
 675 680 685
 Ala Asn Ser Asn Ala Ala Thr Leu Val Leu Gly Leu Pro Lys Asp Phe
 690 695 700
 Gly Met Arg Pro Ile Ser Leu Asp Asn Leu Asp Asp Asn Glu Thr Gly

705	710	715	720
Lys Asn Lys Thr Lys Lys Gly Glu Glu	Thr Pro Leu Lys Glu Glu Ile		
725	730	735	
Glu Glu Phe Arg Gln Lys Arg Gln Ala Ala	Glu Phe Arg Asp Cys Gly		
740	745	750	
Leu Val Asp Leu Leu Asn Gly Thr Tyr Lys Ser Thr Val Val Ile Gln			
755	760	765	
Thr Asn Asn Leu Gly Ile Pro Gly Leu Val Thr Ser Met Asp Gln Leu			
770	775	780	
Tyr Glu Val Ser Cys Asp Tyr Ser Ser Met	Leu Gly Gly Arg Val Gln		
785	790	795	800
Ala Gly Tyr Asn Met Thr Val Thr Gly Pro Glu Ala Asn Leu Ile Gln			
805	810	815	
Pro Arg Gly Lys Ile Glu Leu Gly Asn Pro Val Leu Met Gln Leu Leu			
820	825	830	
Asn Gly Asp Gly Thr Glu Gln Pro Leu Val Gln Ala Lys Leu Gly Asp			
835	840	845	
Ile Leu Glu Leu Arg Trp Glu Ile Met Ala Met Asp Asp Glu Leu Asp			
850	855	860	
Phe Phe Val Lys Asn Cys His Ala Glu Pro Gly Leu Ala Gly Gly Lys			
865	870	875	880
Ala Gly Ala Gly Glu Lys Leu Gln Leu Ile Asp Gly Gly Cys Pro Thr			
885	890	895	
Pro Ala Val Ala Gln Lys Leu Ile Pro Gly Ala Ile Glu Val Lys Ser			
900	905	910	
Ser Ala Val Lys Thr Thr Lys Met Gln Ala Phe Arg Phe Asp Ser Ser			
915	920	925	
Ala Ser Ile Arg Val Thr Cys Glu Val Glu Ile Cys Lys Gly Asp Cys			
930	935	940	
Glu Ala Val Glu Cys Ala Leu Thr Gly Gly Val Lys Lys Ser Phe Gly			
945	950	955	960
Arg Lys Lys Arg Glu Val Asn Asn Ile Glu Glu Phe Glu Thr Asn			
965	970	975	
Arg Tyr Leu Ile Pro Arg Arg Ser His Ala Thr Thr Ser Ile Val Ile			
980	985	990	
Ile Asp Pro Leu Gln Gln Val Asn Glu Pro Val Ala Met Ser Arg Ala			
995	1000	1005	
Ser Thr Leu Asp Leu Leu Arg Glu Glu Ala His Glu Val Gln Val Ile			
1010	1015	1020	
Glu Glu Gly Ser Ile Cys Leu Asn Arg Ile Thr Val Phe Ala Ile Phe			
1025	1030	1035	1040
Gly Thr Leu Ala Val Leu Ile Leu Gly Gln Val Ile Val Val Ala His			
1045	1050	1055	
Tyr Ala Val Arg Arg Phe Ser Thr Glu Lys Thr Ala			
1060	1065		

<210> 46

<211> 742

<212> PRT

<213> Caenorhabditis briggsae

<400> 46

Met Ser Pro Arg Val Ile Phe Leu Leu Gly Ser Phe Leu Thr Ala			
1	5	10	15

Gln Ala Val Phe Glu Cys Ser Ser His Glu Thr Thr Ala Phe Val Arg			
20	25	30	

Ile Pro Arg Ala Arg Leu Asp Gly Thr Pro Val Val Ile Ser Thr Ala			
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35	40	45
Gly His Asp Leu Thr Cys Ala Gln Tyr Cys Arg Asn Asn Ile Glu Pro		
50	55	60
Thr Thr Gly Ala Gln Arg Val Cys Ala Ser Phe Asn Phe Asp Gly Arg		
65	70	75
Glu Thr Cys Tyr Phe Phe Asp Asp Ala Ala Thr Pro Ala Gly Thr Ser		
85	90	95
Gln Leu Thr Ala Asn Pro Ser Ala Asn Asn Phe Tyr Tyr Glu Lys Thr		
100	105	110
Cys Ile Pro Asn Val Ser Ala His Glu Ala Cys Thr Tyr Arg Ser Phe		
115	120	125
Ser Phe Glu Arg Ala Arg Asn Thr Gln Leu Glu Gly Phe Val Lys Lys		
130	135	140
Ser Val Thr Val Lys Asn Arg Glu His Cys Leu Ser Ala Cys Leu Lys		
145	150	155
Glu Lys Glu Phe Val Cys Lys Ser Val Asn Phe His Tyr Glu Asn Ser		
165	170	175
Leu Cys Glu Leu Ser Val Glu Asp Lys Arg Ser Lys Pro Thr His Val		
180	185	190
Arg Met Ser Glu Gly Ile Asp Tyr Tyr Asp Asn Asn Cys Leu Ser Arg		
195	200	205
Gln Asn Arg Cys Gly Pro Ser Gly Gly Asn Leu Val Phe Val Lys Thr		
210	215	220
Thr Asn Phe Glu Ile Arg Tyr Tyr Asp His Thr Gln Ser Val Glu Ala		
225	230	235
Gln Glu Ser Tyr Cys Leu Gln Lys Cys Leu Asp Ser Leu Asn Thr Phe		
245	250	255
Cys Arg Ser Val Glu Phe Asn Pro Lys Glu Lys Asn Cys Ile Val Ser		
260	265	270
Asp Glu Asp Thr Phe Ser Arg Ala Asp Gln Gln Gly Gln Val Val Gly		
275	280	285
Lys Asp Tyr Tyr Glu Pro Ile Cys Val Ala Ala Asp Leu Ser Ser Ser		
290	295	300
Thr Cys Arg Gln Gln Ala Ala Phe Glu Arg Phe Ile Gly Ser Ser Ile		
305	310	315
Glu Gly Glu Val Val Ala Ser Ala Gln Gly Val Thr Ile Ser Asp Cys		
325	330	335
Ile Ser Leu Cys Phe Gln Asn Leu Asn Cys Lys Ser Ile Asn Tyr Asp		
340	345	350
Arg Thr Ala Ser Ser Cys Phe Ile Tyr Ala Val Gly Arg Gln Asp Ala		
355	360	365
Asn Ile Lys Ala Asn Pro Ser Met Asp Tyr Tyr Glu Phe Asn Cys Glu		
370	375	380
Ser Gln Phe Gly Gly Met Ala Leu Cys Thr Asn Glu Gly Ile Arg Phe		
385	390	395
Ile Val Asn Thr Lys Glu Pro Tyr Thr Gly Ala Ile Tyr Ala Ala Glu		
405	410	415
Arg Phe Ser Thr Cys Ser Gln Val Val Glu Asn Ala Lys Gln Ile Ser		
420	425	430
Ile Thr Phe Pro Pro Thr Val Thr Ser Asp Cys Gly Thr Val Ile		
435	440	445
Arg Asp Gly Lys Met Glu Ala Leu Val Val Val Ser Leu Asp Gly Val		
450	455	460
Leu Pro His Gln Val Thr Thr Glu Trp Asp Arg Phe Tyr Arg Val Ser		
465	470	475
Cys Asp Val Ser Met Asp Lys Met Val Lys Glu Gly Ser Val Val Val		
485	490	495

Thr Thr Ile Tyr Glu Ala Ser Ser Gln Asn Thr Thr Val Leu Asp Val
 500 505 510
 Ala Thr Pro Pro Pro Val Thr Ala Glu Leu Gln Ile Leu Asn Gln Leu
 515 520 525
 Glu Glu Pro Leu His Lys Ala Ser Ile Gly Asp Pro Leu Leu Leu Val
 530 535 540
 Ile Thr Ser Glu Gln Ala Gly Pro His Asn Met Met Val Thr Glu Cys
 545 550 555 560
 Thr Ala Thr Arg Val Gly Gly Phe Gly Asp Thr Val Pro Phe Thr Leu
 565 570 575
 Ile Glu Asn Gly Cys Pro Arg Tyr Pro Ala Leu Val Gly Pro Val Glu
 580 585 590
 Gln Asp Phe Asp Lys Asn Arg Leu Lys Ser Asp Leu Arg Ala Phe Arg
 595 600 605
 Leu Asp Gly Ser Tyr Asp Val Gln Ile Val Cys Ser Ile Met Phe Cys
 610 615 620
 Ala Gly Pro Asn Gly Cys Pro Val Ser Asn Cys Leu Asp Ser Gly Thr
 625 630 635 640
 Asn Glu Leu Phe Met Ser His Gly Arg Lys Lys Arg Ser Val Asp Leu
 645 650 655
 Glu Ala Gly Glu Thr Glu Glu Arg Leu Ser Ala Ile Ile Arg Val Phe
 660 665 670
 Ala Lys Gly Glu Asp Glu Glu Ile Glu Met Gly Asn Asn Thr Leu
 675 680 685
 Met Thr Ser Leu Ala Glu Ser Thr Asp Leu Leu Cys Ile Ala Glu Pro
 690 695 700
 Phe Phe Val Ser Ser Val Val Ser Leu Ser Val Leu Cys Phe Ala Leu
 705 710 715 720
 Ser Ala Ile Ile Ala Ile Trp Gly Cys His Ala Leu His Ala Lys Pro
 725 730 735
 Thr Lys Gln Val Ala Ala
 740

<210> 47
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 47
 gtaatacgcac tcactatagg gc

22

<210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 48
 aatataaccct cactaaagg

20

<210> 49
 <211> 19

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 49		
gatttaggtg acactata	19	19
<210> 50		
<211> 29		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 50		
ggccacgcgt cgactagta	29	29
gggggggggg		
<210> 51		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 51		
tcagtgacgt tatgtc	20	20
cctcc		
<210> 52		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 52		
tgacagatgg aacattctcc	20	20
<210> 53		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 53		
acttcaggac acgacttgac	20	20
<210> 54		
<211> 20		
<212> DNA		
<213> Artificial Sequence		

<220>

<223> Primer

<400> 54

caatcagaga tggtaactcc

20